

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Nelson, Edward L.
Nelson, Peter J.
- (ii) TITLE OF INVENTION: NOVEL VECTOR FOR
POLYNUCLEOTIDE VACCINES
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/14306
 - (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US60/023931
 - (B) FILING DATE: 14-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KATHRYN M. BROWN
 - (B) REGISTRATION NUMBER: 34556
 - (C) REFERENCE/DOCKET NUMBER: 2026-4236US1
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 - (A) TELEPHONE: (212) 758-4800
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 - (C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCGCGTTG	CTGGCGTTT	TCCATAGGCT	CCGCC	CCCCCT	40
GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC		80
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTT	CCCC	120
TGGAAGCTCC	CTCGTGCCT	CTCCTGTTCC	GACCC	TGCCG	160
CTTACCGGAT	ACCTCTCCGC	CTTCTCCCT	TCGGGAAGCG		200
TGGCGCTTTC	TCAATGCTCA	CGCTGTAGGT	ATCTCAGTTC		240
GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA		280
CCCCCCGTTTC	AGCCCGACCG	CTGCGCCTTA	TCCGGTA	ACT	320
ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATGCC		360
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG		400
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA		440
ACTACGGCTA	CAC				453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG		40
CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT		80
GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG		120
GACTCAAGAC	GATAAGTAC	GGATAAGGCG	CAGCGGTGCG		160
GCTGAACGGG	GGGTTCGTGC	ACACAGCCC	GCTTGGAGCG		200
AACGACCTAC	ACCGAACTGA	GATAACCTACA	CCGTGAGCAT		240
TGAGAAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGCAGGACA		280
GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC		320
GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT		360
CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT		400
TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC		440
CAGCAACGCG	GCC				453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

GAATTCTTTC	GGACTTTGA	AAGTGATGGT	GGTGGCCGAA	40
GGATTCAAC	CTTCGAAGTC	GATGACGGCA	GATTTAGAGT	80
CTGCTCCCTT	TGGCCGCTCG	GBAACCCCCAC	CACGGGTAAT	120
GCTTTTACTG	GCCTGCTCCC	TTATCAGGAA	GCAGGGCGCA	160
TCATATCAAA	TGACGCGCCG	CTGTAAAGTG	TTACGTTGAG	200
AAAGAATTTC				209

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC	TCAACGTAAC	ACTTTACAGC	GGCGCGTCAT	40
TTGATATGAT	GCGCCCCGCT	TCCCGATAAG	GGAGCAGGCC	80
AGTAAAAGCA	TTACCCGTGG	TGGGGTTCCC	GAGCGGCCAA	120
AGGGAGCAGA	CTCTAAATCT	GCCGTCAATCG	ACTTCGAAGG	160
TTCGAATCCT	TCCCCCACCA	CCATCACTTT	CAAAGTCCG	200
AAAGAATTTC				209

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA

6

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

ATTAAA

6

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA

6

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC

6

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

AATACA

6

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

GCCTTAAGGG	CCATATGGTG	AGTGGATCCC	TTGACCCCAG	40
CGGGGGATGG	GGAGACCTGT	AGTCAGAGCC	CCCGGGCAGC	80
ACAGGCCAAT	GCCC GT C C T T	CCCCTGCAGG	ATGAGTAGTG	120
AGTGCCTCTC	CTGGCCCTGG	AAGTTGCCAC	TCCAGTGCCC	160
ACCAGCCTTG	TCCTAATAAA	ATTAAGTTGC	ATCATTGTTGT	200
CTGACTAGGT	GTCCTCTATA	ATATTAT		227

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAATATTAT	AGAGGACACC	TAGTCAGAAC	AAATGATGCA	40
ACTTAATTTT	ATTAGGACAA	GGCTGGTGGG	CACTGGAGTG	80
GCAACTTCCA	GGGCCAGGAG	AGGCACTCAC	TACTCATCCT	120
GCAGGGGAAG	GACGGGCATT	GCCCTGTGCT	GCCCCGGGGC	160
TCTGACTACA	GGTCTCCCCC	ATCCCCGCT	GGGGTCAAGG	200
CATCCACTCA	CCATATGGCC	CTTAAGG		227

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCGGTACC	TGCCATGGCG	CGGATTCTTT	ATCACTGATA	40
AGTTGGTCCA	CATATTATGT	TTATCAGTGA	TAAAGTGTCA	80
AGCATGACAA	AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	120
GCCCTGGACT	GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	160
GACACGCAA	CTGGCGAAC	GGTTGGGGGT	GCAGCAGCCG	200
GCGCTTTACT	GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	240
GGCCATATGC	CG			252

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT

35

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGT CCTGAAGT

38

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTTAAGGG CCATATGGTG AGTGGATGCC TTGACCCCAG
GCGGGGATGG GGGAGACCTG TAGTCAGAGC CCCCGGGCAG

40
80

CACAGGCCAA TGCCCCTGCAG GATGAGTAGT
GAGTGCCTCT CCTGGCCCTG GAAGTTGCCA CTCCAGTGCC
CACCAAGCCTT GTCCTAAATAA AATTAAGTTG CATCATTTG
TCTGACTAGG TGTCTCTAT AATATTAT

120
160
200
228

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCCATGGCG	CGGATTCTTT	ATCACTGATA	AGTTGGTGGA	40
CATATTATGT	TTATCAGTGA	TAAAGTGTCA	AGCATGACAA	80
AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	GCCCTGGACT	120
GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	GACACGCAAA	160
CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	GCGCTTTACT	200
GGCACCTTCAG	GAACAAGCGG	GCGCCTTAAG	GGCCATATGG	240
TGAGTGGATG	CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	280
TGTAGTCAGA	GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	320
CTTCCCTCTGC	AGTGAGTAGT	GACTGCCCGG	GTGGGATCCC	360
TGTGACCCCT	CCCCAGTGCC	TCTCCTGGCC	CTGGAAGTTG	400
CCACTCCAGT	GCCCACCAAGC	CTTGTCTCAA	TAAAATTAAG	440
TTGCATCATT	TTGTCTGACT	AGGTGTCCCTC	TATAATATTA	480
TAAGCTTGAT	ATCGAATTCT	TTCTCAACGT	AACACTTTAC	520
AGCGGCGCGT	CATTGATAT	GATGCGCCCC	GCTTCCCGAT	560
AAGGGAGCAG	GCCAGTAAAA	GCATTACCCG	TGGTGGGGTT	600
CCCGAGCGGC	CAAAGGGAGC	AGACTCTAAA	TCTGCCGTCA	640
TCGACTTCGA	AGGTTCGAAT	CCTTCCCCCA	CCACCATCAC	680
TTTCAAAAGT	CCGAAAGAAT	TCCTGCAGCC	CGTGTAGCCG	720
TAGTTAGGCC	ACCACTTCAA	GAACTCTGTA	GCACCGCCTA	760
CATACCTCGC	TCTGCTAATC	CTGTTACCAAG	TGGCTGCTGC	800
CAGTGGCGAT	AAAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	840
CGATAGTTAC	CGGATAAGGC	GCAGCGGTGCG	GGCTGAACGG	880
GGGGTTCGTG	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	920
CACCGAACTG	AGATACCTAC	AGCGTGAGCA	TTGAGAAAGC	960
GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	1000
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	1040
TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG	TCCTGTCGGG	1080
TTTCGCCACC	TCTGACTTGA	GCGTCGATT	TTGTGATGCT	1120
CGTCAGGGGG	GGCGAGCCTA	TGGAAAACG	CCAGCAACGC	1160
GGCCGGGGGA	TCCGGAGAGC	TCACTCTAGA	TGAGAGAGCA	1200
GTGAGGGAGA	GACAGAGACT	CGAATTTCGG	GAGCTATTTC	1240
AGTTTCTTT	TCCGTTTGT	GCAATTTCAC	TTATGATACC	1280
GGCCAATGCT	TGGTTGCTAT	TTTGGAAACT	CCCCTTAGGG	1320
GATGCCCTC	AACTGGCCCT	ATAAAGGGCC	AGCCTGAGCT	1360
GCAGAGGATT	CCTGCAGAGG	ATCAAGACAG	CACGTGGACC	1400
TCGCACAGCC	TCTCCACAG	GTACC		1425

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATGAGCAAGG	GCGAGGAACT	GTTCACTGGC	GTGGTCCCAA	40
TTCTCGTGG	A	C	T	80
TTCTGTCAGC	GGAGAGGGTG	AAGGTGATGC	CACATACGG	120
AAGCTCACCC	TGAAATTCA	CTGCACCACT	GGAAAGCTC	160
CTGTGCCATG	GCCAACACTG	GTCAC	TAC	200
CGTGCAGTGC	TTTTCCAGAT	ACCCAGACCA	TATGAACGAG	240
CATGACTTTT	TCAAGAGCGC	CATGCCGAG	GGCTATGTGC	280
AGGAGAGAAC	CATCTTTTC	AAAGATGACG	GGAACTACAA	320
GACCCGCGCT	GAAGTCAAGT	TCGAAGGTGA	CACCCTGGTG	360
AATAGAATCG	AGTTGAAGGG	CATTGACTTT	AAGGAAGATG	400
GAAACATTCT	CGGCCACAAG	CTGGAATACA	ACTATAACTC	440
CCACAATGTG	TACATCATGG	CCGACAAGCA	AAAGAATGGC	480
ATCAAGGTCA	ACTTCAAGAT	CAGACACAAAC	ATTGAGGATG	520
GATCCGTGCA	GCTGGCCGAC	CATTATCAAC	AGAACACTCC	560
AATCGGCGAC	CGCCCTGTGC	TCCTCCCAGA	CAACAATTAC	600
CTGTCCACCC	AGTCTGCCCT	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGAGCA	CATGGTCCTG	CTGGAGTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGC	719

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

TATGAGCAAG	GGCGAGGAAC	TGTTCACTGG	CGTGGTCCCA	40
ATTCTCGTGG	AACTGGATGG	CGATGTGAAT	GGGCACAAAT	80
TTTCTGTCAG	CGGAGAGGGT	GAAGGGTGTG	CCACATACGG	120
AAAGCTCACC	CTGAAATTCA	TCTGCACCCAC	TGGAAAGCTC	160
CCTGTGCCAT	GGCCAACACT	GGTCACTACC	TTCACCTATG	200
GCGTGCAGTG	CTTTTCCAGA	TACCCAGACC	ATATGAAGCA	240
GCATGACTT	TTCAAGAGCG	CCATGCCCGA	GGGCTATGTG	280
CAGGAGAGAA	CCATCTTTT	CAAAGATGAC	GGGAACATACA	320
AGACCCGCGC	TGAAGTCAAG	TTCGAAGGGT	ACACCCCTGGT	360
GAATAGAAC	GAGTTGAAGG	GCATTGACTT	TAAGGAAGAT	400
GGAAACATTC	TCGGGCCAACAA	GCTGGAATAC	AACTATAACT	440
CCCACAAATGT	GTACATCATG	GGCGAACAGC	AAAAGAATGG	480
CATCAAGGTC	AACTTCAAGA	TCAGACACAA	CATTGAGGAT	520
GGATCCGTGC	AGCTGGCCGA	CCATTATCAA	CAGAACACTC	560
CAATCGCGA	CGGCCCTGTG	CTCCTCCCAG	ACAACCATT	600
CCTGTCCACC	CAGTCTGCC	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCCTG	CTGGAGTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGCC	720
ATATGGTGAG	TGGATGCC	GACCCCAGGC	GGGGATGGGG	760
GAGACCTGTA	GTCAGAGCCC	CCGGGCAGCA	CAGGCCATG	800
CCC GTCCCTC	CCCTGCAGTG	AGTAGTGA	GCCCGGGTGG	840
GATCCCTGTG	ACCCCTCCCC	AGTGCCTCTC	CTGGCCCTGG	880
AAGTTGCCAC	TCCAGTCCCC	ACCAGCCTG	TCCTAATAAA	920
ATTAAGTTGC	ATCATTGTTG	CTGACTAGGT	GTCCCTCTATA	960
ATATTATAAG	CTTGATATCG	AATTCTTCT	CAACGTAACA	1000
CTTTACAGCG	GCGCGTCATT	TGATATGATG	CGCCCCGCTT	1040
CCCGATAAGG	GAGCAGGCCA	GTAAAAGCAT	TACCCGTGGT	1080
GGGGTTCCCG	AGCGGCCAAA	GGGAGCAGAC	TCTAAATCTG	1120
CCGTCATCGA	CTTCGAAGGT	TCGAATCCTT	CCCCCACAC	1160
CATCACTTTC	AAAAGTCCGA	AAGAATTCT	GCAGCCCGTG	1200
TAGCCGTAGT	TAGGCCACCA	CTTCAAGAAC	TCTGTAGCAC	1240
CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCAGTGGC	1280
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	1320
TCAAGACGAT	AGTTACCGGA	TAAGGCGCAG	CGGTGCGGGCT	1360
GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	1400
GACCTACACC	GAAC TGAGAT	ACCTACAGCG	TGAGCATTGA	1440
GAAAGCGCCA	CGCTTCCCAGA	AGGGAGAAAG	CGGGACAGGT	1480
ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	1520
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	1560
GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT	CGATTTTGT	1600
GATGCTCGTC	AGGGGGCGG	AGCCTATGGA	AAAACGCCAG	1640
CAACCGGCC	GGGGGATCCG	GAGAGCTCAC	TCTAGATGAG	1680
AGAGCAGTGA	GGGAGAGACA	GAGACTCGAA	TTTCCGGAGC	1720
TATTCAGTT	TTCTTTCCG	TTTGTGCAA	TTTCACTTAT	1760
GATACCGGCC	AATGCTGGT	TGCTATTTG	GAAACTCCCC	1800
TTAGGGGATG	CCCCTCAACT	GGCCCTATAA	AGGGCCAGCC	1840
TGAGCTGCAG	AGGATTCTG	CAGAGGATCA	AGACAGCACG	1880
TGGACCTCGC	ACAGCCTCTC	CCACAGGTAC	C	1911

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:

Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
1 5 10
Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
15 20
Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly
25 30 35
Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
40 45
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
50 55 60
Val Leu Gly Val Val Phe Gly Ile Leu
65

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg
1 5 10
His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp
15 20
Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala
25 30 35
Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
40 45
Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala
50 55 60
Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser
65 70
Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
75 80
Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
85 90 95

Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
100 105
Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro
110 115 120

Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
125 130
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val
135 140

Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu
145 150 155
Asn Pro Glu Tyr Leu Thr Pro Gln Gly Thr Cys Ser
160 165
Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg
170 175 180
Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
185 190
Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
195 200
Lys Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
205 210 215
Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
220 225
Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro
230 235 240
His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn
245 250
Leu Tyr Tyr Trp Asp Asp Pro Pro Glu Arg Gly Ala
255 260
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu
260 270 275
Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
280 285

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
1 5 10

Val Leu Gly Val Val Phe Gly Ile Leu Ile
15 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCATGG	CCCCTGACCT	CTCCTACATG	CCCATCTGGA	40
AGTTTCCAGA	TGAGGAGGGC	GCATGCCAGC	CTTGCCCCAT	80
CAACTGCACC	CACTCCTGTG	TGGACCTGGA	TGACAAGGGC	120
TGCCCCGCCG	AGCAGAGAGC	CAGCCCTCTG	ACGTCCATCA	160
TCTCTGCGGT	GGTTGGCATT	CTGCTGGTCG	TGGTCTTGGG	200
GGTGGCTTT	GGGATCCTCA	TCAAGCGACG	GCAGCAGAAC	240
ATCACATGTC	CAGACCCCTGC	CCCGGGCGCT	GGGGCATGG	280
TCCACCACAG	GCACCGCAGC	TCATCTACCA	GGAGTGGCGG	320
TGGGGACCTG	ACACTAGGGC	TGGAGCCCTC	TGAAGAGGAG	360
GCCCCCAGGT	CTCCACTGGC	ACCCTCCGAA	GGGGCTGGCT	400
CCGATGTATT	TGATGGTGAC	CTGGGAATGG	GGGCAGCCAA	440
GGGGCTGCAA	AGCCTCCCCA	CACATGACCC	CAGCCCTCTA	480
CAGCGGTACA	GTGAGGACCC	CACAGTACCC	CTGCCCTCTG	520
AGACTGATGG	CTACGTTGCC	CCCCTGACCT	GCAGCCCCCA	560
GCCTGAATAT	GTGAACCAGC	CAGATGTTCG	GCCCCAGCCC	600
CCTTCGCCCC	GAGAGGGCCC	TCTGCCTGCT	GCCCGACCTG	640
CTGGTGCAC	TCTGGAAAGG	CCCAAGACTC	TCTCCCCAGG	680
GAAGAATGGG	GTCGTCAAAG	ACGTTTTGC	CTTGGGGGT	720
GCCGTGGAGA	ACCCCGAGAC	TTGACACCCC	AGGGAGGAGC	760
TGCCCCCTCAG	CCCCACCCCTC	CTCCTGCCTT	CAGCCCAGCC	800
TTCGACAACC	TCTATTACTG	GGACCAGGAC	CCACCCAGAGC	840
GGGGGGCTCC	ACCCAGCACC	TTCAAAGGGA	CACCTACGGC	880
AGAGAACCCA	GAGTACCTGG	GTCTGGACGT	GCCAGTGTGA	920
AGCCTTAAGG	GCCATATGGT	GAGTGGATGC	CTTGACACCCCA	960
GGCGGGGATG	GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	1000
GCACAGGCCA	ATGCCCGTCC	TTCCCCTGCA	GTGAGTAGTG	1040
ACTGCCCGGG	TGGGATCCCT	GTGACCCCTC	CCCAGTGCCT	1080
CTCCTGGCCC	TGGAAGTTGC	CACTCCAGTG	CCACACCAGCC	1120
TTGTCTTAAT	AAAATTAAGT	TGCATCATTT	TGTCTGACTA	1160
GGTGTCCCTCT	ATAATATTAT	AAGCTTGATA	TCGAATTCTT	1200
TCTCAACGTA	ACACTTTACA	GC GGCGCGTC	ATTGATATG	1240
ATGCGCCCCG	CTTCCCGATA	AGGGAGCAGG	CCAGTAAAAG	1280
CATTACCCGT	GGTGGGGTTC	CCGAGCGGCC	AAAGGGAGCA	1320
GAECTAAAT	CTGCCGTCA	CGACTTCGAA	GGTTCGAATC	1360
CTTCCCCCAC	CACCATCACT	TTCAAAAGTC	CGAAAGAATT	1400
CCTGCAGCCC	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1440
AACTCTGTAG	CACCGCTAC	ATACCTCGCT	CTGCTAATCC	1480
TGTTACCAAGT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	1520
TACCGGGTTG	GACTCAAGAC	GATAGTTACC	GGATAAGGCG	1560
CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	1600
GCTTGGAGCG	AACGACCTAC	ACCGAACTGA	GATACTACA	1640
GCGTGAGCAT	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1680
AAGGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTGGGAACAG	1720
GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	1760
TCTTTATAGT	CCTGTGGGT	TTCGCCACCT	CTGACTTGAG	1800
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	1840
GGAAAAAACGC	CAGCAACGCG	GCCGGGGGAT	CCGGAGAGCT	1880
CACTCTAGAT	GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	1920
GAATTCCGG	AGCTATTCA	GT TTTCTTT	CCGTTTGTG	1960

CAATTCACT TATGATACCG GCCAATGCTT GGTTGCTATT	2000
TTGGAAACTC CCCTTAGGGG ATGCCCTCA ACTGGCCCTA	2040
TAAAGGGCCA GCCTGAGCTG CAGAGGATTC CTGCAGAGGA	2080
TCAAGACAGC ACGTGGACCT CGCACAGCCT CTCCCACAGG	2120
TACCT	2125

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

GTCTGCCACC ATGGCCTACT CCCCTGC

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

TTCTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	40
TGAGTCAGGA	AACATTTCA	GACCTATGGA	AACTACTTCC	80
TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTGAA	TGCTGTCCCC	GGACGATATT	GAACAATGGT	160
TCACTGAAGA	CCCAGGTCCA	GATGAAGCTC	CCAGAATGCC	200
AGAGGGCTGCT	CCCCCGCTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCCGGCG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCTGT	280
CATCTTCTGT	CCCTTCCCAG	AAAACCTACC	AGGGCAGCTA	320
CGGTTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGCCACCA	TGGCCTACTC	CCCTGCGTCT	GTGACTTGCA	400
CGTACTCCCC	TGCCCTCAAC	AAAGATGTTT	GCCAACTGGC	440
CAAGACCTGC	CCTGTGCAGC	TGTGGGTTGA	TTCCACACCC	480
CCGCCCCGGCA	CCCGCGTCCG	CGCCATGGCC	ATCTACAAGC	520
AGTCACAGCA	CATGACGGAG	GTTGTGAGGC	GCTGCCCCCA	560
CCATGAGCGC	TGCTCAGATA	GCGATGGTCT	GGCCCCCTCCT	600
CAGCGTCTTA	TCCGAGTGGA	AGGAAATTG	CGTGTGGAGT	640
ATTTGGATGA	CAGAAACACT	TTTCGACATA	GTGTGGTGGT	680
GCCCTATGAG	CCGCCTGAGG	TTGGCTCTGA	CTGTACCAACC	720
ATCCACTACA	ACTACATGTG	TAACAGTTCC	TGCATGGCG	760
GCATGAACCG	GAGGCCCATC	CTCACCATCA	TCACACTGGA	800
AGACTCCAGT	GGTAATCTAC	TGGGACGGAA	CAGCTTGAG	840
GTGCGTGTGTT	GTGCCTGTCC	TGGGAGAGAC	CGGGCGCACAG	880
AGGAAGAGAA	TCTCCGCAAG	AAAGGGGAGC	CTCACCAACGA	920
GCTGCCCA	GGGAGCACTA	AGCGAGCACT	GCCCAACAAAC	960
ACCAAGCTCCT	CTCCCCCAGCC	AAAGAAGAAA	CCACTGGATG	1000
GAGAATATTT	CACCCCTTCAG	ATCCGTGGGC	GTGAGCGCTT	1040
CGAGATGTTC	TTTGGTGACC	TACCTCTTCG	GAATTGCCGA	1080
GTCTTCCGAG	AGCTGAATGA	GGCCTTGGAA	CTCAAGGATG	1120
CCCAGGCTGG	GAAGGAGCCA	GGGGGGAGCA	GGGCTCACTC	1160
CAGCCACCTG	AAGTCCAAAA	AGGGTCAGTC	TACCTCCCAC	1200
CATAAAAAAC	TCATGTTCAA	GACAGAAGGG	CCTGACTCAG	1240
AC				1242

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCGGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCC	40
CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	80
TGGCGAAACC	CGACAGGACT	ATAAAGATAC	CAGGGCGTTTC	120
CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCCT	160
GCCGCTTACCC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	200
AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	240
GTTCGGTGTA	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	280
CGAACCCCCC	GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	320
AACTATCGTC	TTGAGTCAA	CCCGGTAAGA	CACGACTTAT	360
CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	400
GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	440
CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	480
GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	520
TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	560
GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAAA	600
	AAGGATCT			608

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATAACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACCGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTTACTG	GCACTTCAAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCCA	GGCGGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCGTCC	TTCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAAGCCT	400
TGTCCTAATA	AAATTAAGTT	GCATCATTTC	GTCTGACTAG	440
GTGTCCCTCA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCCA	CCACGGGTAA	TGCTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGGCGC	ATCATATCAA	640
ATGACCGGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTG	680
CTGCAGCCCG	GGCGTGTGCT	GGCGTTTTTC	CATAGGCTCC	720

GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GAECTATAAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTCGG	TGTAGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTCAG	CCCGACCGCT	GCCCTTATC	1000
CGGTAACTAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGGGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTGTTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAAGGAT	CTGGGGGATC	CGGAGAGGCTC	ACTCTAGATG	1320
AGAGAGCAGT	GAGGGAGAGA	CAGAGACTCG	AATTTCCGGA	1360
GCTATTTCA	TTTTCTTTTC	CGTTTTGTGC	AATTTCACTT	1400
ATGATACCGG	CCAATGTTG	GTTGCTATTT	TGGAAACTCC	1440
CCTTAGGGGA	TGCCCCCTCAA	CTGGCCCTAT	AAAGGGCCAG	1480
CCTGAGCTGC	AGAGGATTCC	TGCAGAGGAT	CAAGACAGCA	1520
CGTGGACCTC	GCACAGCCTC	TCCCACAA		1547

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:28:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACGGAG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTAACTG	GCACTTCAAG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCGTCC	TTCCCCCTGCA	GGATGAGTAG	TGAGTGCCTC	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCTTAATA	AAATTAAGTT	GCATCATTTC	GTCTGACTAG	440
GTGTCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTGCAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCA	CCACGGGTAA	TGCTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTG	680

CTGCAGCCCG	CCGCGTTGCT	GGCGTTTTC	CATAGGCTCC	720
GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCTG	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTCAAG	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACATAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTGCA	AGCAGCAGAT	TACGCCGAGA	1280
AAAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	CCAACCGCGTT	1320
GGATGCATGG	ATGAGGGAAA	GGAGGTAAGA	TCTGTAATGA	1360
ATAAGCAGGA	ACTTTGAAGA	CTCAGTGACT	CAGTGAGTAA	1400
TAAAGACTCA	GTGACTTCTG	ATCCTGTCTC	AACTGCCACT	1440
CCTTGTGTC	CCAAGAAAGC	GGCTTCCTGC	TCTCTGAGGA	1480
GGACCCCTTC	CCTGGAAGGT	AAAACTAAGG	ATGTCAGCAG	1520
AGAAATTTTT	CCACCATTTGG	TGCTTGGTCA	AAGAGGAAAC	1560
TGATGAGCTC	ACTCTAGATG	AGAGAGCAGT	GAGGGAGAGA	1600
CAGAGACTCG	AATTTCCGGA	GCTATTTCA	TTTCTTTTC	1640
CGTTTTGTGC	AATTTCACTT	ATGATACCGG	CCAATGCTTG	1680
GTTGCTATTT	TGGAAACTCC	CCTTAGGGGA	TGCCCTCAA	1720
CTGGCCCTAT	AAAGGGCCAG	CCTGAGCTGC	AGAGGATTCC	1760
TGCAGAGGAT	CAAGACAGCA	CGTGGACCTC	GCACAGCCTC	1800
TCCCCACA				1807

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTACCTGCC	ACCATGGCGA	AGGGCGAGGA	ACTGTTCACT	40
GGCGTGGTCC	CAATTCTCGT	GGAACTGGAT	GGCGATGTGA	80
ATGGGCACAA	ATTTTCTGTC	AGCGGAGAGG	GTGAAGGTGA	120
TGCCACATAC	GGAAAGCTCA	CCCTGAAATT	CATCTGCACC	160
ACTGGAAAGC	TCCCTGTGCC	ATGGCCAACA	CTGGTCACTA	200
CCTTCACCTA	TGGCGTGCAG	TGCTTTCCA	GATAACCCAGA	240
CCATATGAAG	CAGCATGACT	TTTTCAAGAG	CGCCATGCC	280

GAGGGCTATG	TGCAGGAGAG	AACCATCTT	TTCAAAGATG	320
ACGGGAACTA	CAAGACCCGC	GCTGAAGTC	AGTTCGAAGG	360
TGACACCCCTG	GTGAATAGAA	TCGAGTTGAA	GGGCATTGAC	400
TTTAAGGAAG	ATGGAAACAT	TCTCGGCCAC	AAGCTGGAAT	440
ACAACATATAA	CTCCCCACAAT	GTGTACATCA	TGGCCGACAA	480
GCAAAAGAAC	GGCATCAAGG	TCAACTTCAA	GATCAGACAC	520
AACATTGAGG	ATGGATCCGT	GCAGCTGGCC	GACCATTATC	560
AACAGAACAC	TCCAATCGGC	GACGGCCCTG	TGCTCCTCCC	600
AGACAACCAT	TACCTGTCCA	CCCAGTCTGC	CCTGTCTAAA	640
GATCCCAACG	AAAAGAGAGA	CCACATGGTC	CTGCTGGAGT	680
TTGTGACCGC	TGCTGGGATC	ACACATGGCA	TGGACGAGCT	720
GTACAAGTGA	GCGCCTTAAG	GGCCATATGG	TGAGTGGATG	760
CCTTGACCCCC	AGGCGGGGAT	GGGGGAGACC	TGTAGTCAGA	800
GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	CTTCCCCCTGC	840
AGGATGAGTA	GTGAGTGCCT	CTCCTGGCCC	TGGAAGTTGC	880
CACTCCAGTG	CCCACCAAGCC	TTGTCTTAAT	AAAATTAAGT	920
TGCATCATTT	TGTCTGACTA	GGTGTCTCT	ATAATATTAT	960
AAGCTTGATA	TCGAATTCTT	TCGGACTTTT	GAAAGTGTG	1000
GTGGTGGGGG	AAGGATTCGA	ACCTTCGAAG	TCGATGACGG	1040
CAGATTAGA	GTCTGCTCCC	TTTGGCCGCT	CGGGAACCCC	1080
ACCACGGGTA	ATGCTTTTAC	TGGCCTGCTC	CCTTATCGGG	1120
AAGCGGGGCG	CATCATATCA	AATGACGCGC	CGCTGTAAAG	1160
TGTTACGTTG	AGAAAGAATT	CCTGCAGGCC	GCCCGTGTGC	1200
TGGCGTTTTT	CCATAGGCTC	CGCCCCCCTG	ACGAGCATCA	1240
CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	1280
GGACTATAAA	GATACCAGGC	TTTCCCCCT	GGAAGCTCCC	1320
TCGTGCGCTC	TCCTGTTCCG	ACCCTGCCGC	TTACCGGATA	1360
CCTGTCCGCC	TTTCTCCCTT	CGGGAAGCGT	GGCGCTTTCT	1400
CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCG	GTGTAGGTGC	1440
TTCGCTCCAA	GCTGGCTGT	GTGCACGAAC	CCCCCGTTCA	1480
GCCCCGACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	1520
TCCAACCCGG	TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	1560
CCACTGGTAA	CAGGATTAGC	AGAGCGAGGT	ATGTAGGCAG	1600
TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	1640
ACTAGAAGGA	CAGTATTG	TATCTGCGCT	CTGCTGAAGC	1680
CAGTTACCTT	CGGAAAAAGA	GTGGTAGCT	CTTGATCCGG	1720
CAAACAAACC	ACCGCTGGTA	CGGGTGGTTT	TTTGTTTGC	1760
AAGCAGCAGA	TTACGCGCAG	AAAAAAAGGA	TCTGGGGGAT	1800
CCGGGAGAGCT	CCCAACCGT	TGGATGCATG	GATGAGGGAA	1840
AGGAGGTAAG	ATCTGTAATG	AATAAGCAGG	AACTTTGAAG	1880
ACTCAGTGAC	TCAGTGAGTA	ATAAAGACTC	AGTGAATTCT	1920
GATCCTGTCC	TAACTGCCAC	TCCTTGTGT	CCCAAGAAAG	1960
CGGCTTCCTG	CTCTCTGAGG	AGGACCCCTT	CCCTGGAAGG	2000
TAAAACATAAG	GATGTCAGCA	GAGAAATTTC	TCCACCATTG	2040
GTGCTTGGTC	AAAGAGGAAA	CTGATGAGCT	CACTCTAGAT	2080
GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	GAATTTCCGG	2120
AGCTATTTCA	GTTTCTTTT	CCGTTTTGTG	CAATTCACT	2160
TATGATACCG	GCCAATGCTT	GGTTGCTATT	TTGGAAACTC	2200
CCCTTAGGGG	ATGCCCTCA	ACTGGCCCTA	AAAAGGGCCA	2240
GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	TCAAGACAGC	2280
ACGTGGACCT	CGCACAGCCT	CTCCCCACA		2308